38. The method according to claim 37, wherein the rRNA is selected from the group consisting of precursor rRNA and 23S, 16S, and 5S rRNA.

39. The method according to claim 37 for detecting a target sequence of one or more mycobacteria of the *Mycobacterium tuberculosis* Complex (MTC).

40. The method according to claim 39, wherein the mycobacteria is selected from the group consisting of *M. tuberculosis*, *M. bovis*, *M. africanum*, and *M. microti*.

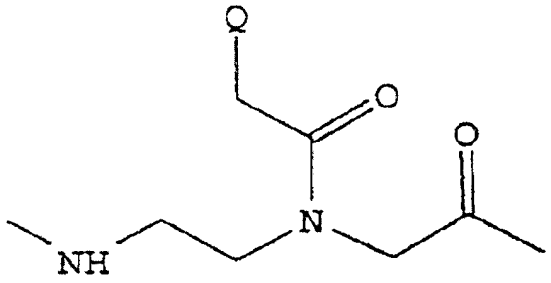
41. The method according to claim 37 for detecting a target sequence of one or more mycobacteria other than mycobacteria of the *Mycobacterium tuberculosis* Complex (MOTT).

42. The method according to claim 41, wherein the mycobacteria other than mycobacteria of the *Mycobacterium tuberculosis* Complex (MOTT) is selected from the group consisting of *M. avium, M. intracellulare, M. kansasii, M. gordonae, M. scrofulaceum, M. xenopi* and *M. fortuitum*.

43. The method according to claim 37, wherein the hybridisation takes place in situ.

44. The method according to claim 37 wherein the hybridisation takes place in vitro.

45. The method according to claim 37, wherein the peptide nucleic acid probe comprises polymerised moieties of the formula (V)



(V)

wherein Q is a nucleobase selected from the group consisting of thymine, adenine, cytosine, guanine, uracil, iso-C, and 2,6-diaminopurine.

46. The method according to claim 37, wherein a signal amplifying system is used for measuring any detectable hybrids.

47. The method according to claim 37, wherein the sample is a sputum sample.